==
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=12; day=18; hr=15; min=25; sec=51; ms=357;
]
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Application No: 10552949   Version No: 1.0

                    Input Set:

                    Output Set:

                      Started: 2008-12-01 18:51:30.378
                     Finished: 2008-12-01 18:51:31.157
                      Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 779 ms
             Total Warnings: 9
               Total Errors: 0
       No. of SeqIDs Defined: 9
         Actual SeqID Count: 9

Error code   Error Description

W   402   Undefined organism found in <213> in SEQ ID (1)

W   402   Undefined organism found in <213> in SEQ ID (2)

W   402   Undefined organism found in <213> in SEQ ID (3)

W   402   Undefined organism found in <213> in SEQ ID (4)

W   402   Undefined organism found in <213> in SEQ ID (5)

W   402   Undefined organism found in <213> in SEQ ID (6)

W   402   Undefined organism found in <213> in SEQ ID (7)

W   402   Undefined organism found in <213> in SEQ ID (8)

W   402   Undefined organism found in <213> in SEQ ID (9)

<110> Omary, Bishr
     Ku, Nam-Om

<120> Keratin 8 and 18 mutations are Risk
  Factors for Developing Liver Disease of Multiple Etiologies

<130> STAN-297WO

<140> 10552949
<141> 2008-12-01

<150> 60/462,989
<151> 2003-04-14

<160> 9

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (119)...(1408)

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ccgccaccgt cgtccgcaaa gcctgagtcc tgtcctttct ctctccccgg acagcatg   118
agc ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc   166
Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly
 1   5   10   15

tct gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc   214
Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala
          20   25   30

agc gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc   262
Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser
       35   40   45

cgc tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc   310
Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr
    50   55   60

ggg ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag   358
Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys
 65   70   75   80

gag acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga   406
Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg

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                    85                    90                    95

gtg agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg        454
Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg
            100                 105                 110

gag cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac        502
Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr
            115                 120                 125

ttc aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg        550
Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val
            130                 135                 140

gac aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct        598
Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala
145                 150                 155                 160

gat gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct        646
Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser
                165                 170                 175

gtg gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat        694
Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn
            180                 185                 190

atc aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag        742
Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu
            195                 200                 205

ctg ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa        790
Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln
            210                 215                 220

gcc cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa        838
Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys
225                 230                 235                 240

tct cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac        886
Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp
                245                 250                 255

gag ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag        934
Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln
            260                 265                 270

cag att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt        982
Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val
            275                 280                 285

gga gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc       1030
Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser
            290                 295                 300

ttg gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag       1078
Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu
305                 310                 315                 320
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aac agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag        1126
Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln
            325                 330                 335

ctc aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg        1174
Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg
            340                 345                 350

gca gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc        1222
Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile
        355                 360                 365

aag gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa        1270
Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu
        370                 375                 380

gat ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc        1318
Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser
385                 390                 395                 400

atg caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa        1366
Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys
                405                 410                 415

gtg gtg tct gag acc aat gac acc aaa gtt ctg agg cat taa              1408
Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His  *
            420                 425

gccagcagaa gcagggtacc ctttggggag caggaggcca ataaaaagtt cagagttcaa        1468
aaaaaaaaaa aaaaaaa                                                   1485


<210> 2
<211> 429
<212> PRT
<213> H. sapiens

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            20                  25                  30
Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser
            35                  40                  45
Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr
        50                  55                  60
Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys
65                  70                  75                  80
Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg
                85                  90                  95
Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg
            100                 105                 110
Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr
        115                 120                 125
Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val
        130                 135                 140
Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala
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```
                145                     150                     155                     160
Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser
                    165                     170                     175
Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn
                180                     185                     190
Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu
            195                     200                     205
Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln
        210                     215                     220
Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys
225                     230                     235                     240
Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp
                245                     250                     255
Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln
                260                     265                     270
Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val
            275                     280                     285
Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser
        290                     295                     300
Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu
305                     310                     315                     320
Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln
                325                     330                     335
Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg
                340                     345                     350
Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile
            355                     360                     365
Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu
        370                     375                     380
Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser
385                     390                     395                     400
Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys
                405                     410                     415
Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His
            420                     425
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ctgctccttc taggatctcc gcctggttcg gcccgcctgc ctccactcct gcctccacca      60

tg tcc atc agg gtg acc cag aag tcc tac aag gtg tcc acc tct ggc        107
   Ser Ile Arg Val Thr Gln Lys Ser Tyr Lys Val Ser Thr Ser Gly
    1               5                   10                  15


ccc cgg gcc ttc agc agc cgc tcc tac acg agt ggg ccc ggt tcc cgc      155
Pro Arg Ala Phe Ser Ser Arg Ser Tyr Thr Ser Gly Pro Gly Ser Arg
                20                  25                  30


atc agc tcc tcg agc ttc tcc cga gtg ggc agc agc aac ttt cgc ggt      203
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Ile Ser Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly
         35                  40                  45


ggc ctg ggc ggc ggc tat ggt ggg gcc agc ggc atg gga ggc atc acc       251
Gly Leu Gly Gly Gly Tyr Gly Gly Ala Ser Gly Met Gly Gly Ile Thr
         50                  55                  60


gca gtt acg gtc aac cag agc ctg ctg agc ccc ctt gtc ctg gag gtg       299
Ala Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val
         65                  70                  75


gac ccc aac atc cag gcc gtg cgc acc cag gag aag gag cag atc aag       347
Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys
 80                  85                  90                  95


acc ctc aac aac aag ttt gcc tcc ttc ata gac aag gta cgg ttc ctg       395
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
                    100                 105                 110


gag cag cag aac aag atg ctg gag acc aag tgg agc ctc ctg cag cag       443
Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln
                115                 120                 125


cag aag acg gct cga agc aac atg gac aac atg ttc gag agc tac atc       491
Gln Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile
            130                 135                 140


aac aac ctt agg cgg cag ctg gag act ctg ggc cag gag aag ctg aag       539
Asn Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys
        145                 150                 155


ctg gag gcg gag ctt ggc aac atg cag ggg ctg gtg gag gac ttc aag       587
Leu Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys
160                 165                 170                 175


aac aag tat gag gat gag atc aat aag cgt aca gag atg gag aac gaa       635
Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Thr Glu Met Glu Asn Glu
                180                 185                 190


ttt gtc ctc atc aag aag gat gtg gat gaa gct tac atg aac aag gta       683
Phe Val Leu Ile Lys Lys Asp Val Asp Glu Ala Tyr Met Asn Lys Val
                195                 200                 205


gag ctg gag tct cgc ctg gaa ggg ctg acc gac gag atc aac ttc ctc       731
Glu Leu Glu Ser Arg Leu Glu Gly Leu Thr Asp Glu Ile Asn Phe Leu
            210                 215                 220


agg cag cta tat gaa gag gag atc cgg gag ctg cag tcc cag atc tcg       779
Arg Gln Leu Tyr Glu Glu Glu Ile Arg Glu Leu Gln Ser Gln Ile Ser
        225                 230                 235


gac aca tct gtg gtg ctg tcc atg gac aac agc cgc tcc ctg gac atg       827
Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp Met
240                 245                 250                 255


gac agc atc att gct gag gtc aag gca cag tac gag gat att gcc aac       875
Asp Ser Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Asp Ile Ala Asn
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cgc agc cgg gct gag gct gag agc atg tac cag atc aag tat gag gag        923
Arg Ser Arg Ala Glu Ala Glu Ser Met Tyr Gln Ile Lys Tyr Glu Glu
        275                    280                    285

ctg cag agc ctg gct ggg aag cac ggg gat gac ctg cgg cgc aca aag        971
Leu Gln Ser Leu Ala Gly Lys His Gly Asp Asp Leu Arg Arg Thr Lys
        290                    295                    300

act gag atc tct gag atg aac cgg aac atc agc cgg ctc cag gct gag       1019
Thr Glu Ile Ser Glu Met Asn Arg Asn Ile Ser Arg Leu Gln Ala Glu
    305                    310                    315

att gag ggc ctc aaa ggc cag agg gct tcc ctg gag gcc gcc att gca       1067
Ile Glu Gly Leu Lys Gly Gln Arg Ala Ser Leu Glu Ala Ala Ile Ala
320                    325                    330                    335

gat gcc gag cag cgt gga gag ctg gcc att aag gat gcc aac gcc aag       1115
Asp Ala Glu Gln Arg Gly Glu Leu Ala Ile Lys Asp Ala Asn Ala Lys
                340                    345                    350

ttg tcc gag ctg gag gcc gcc ctg cag cgg gcc aag cag gac atg gcg       1163
Leu Ser Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
        355                    360                    365

cgg cag ctg cgt gag tac cag gag ctg atg aac gtc aag ctg gcc ctg       1211
Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu
        370                    375                    380

gac atc gag atc gcc acc tac agg aag ctg ctg gag ggc gag gag agc       1259
Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser
    385                    390                    395

cgg ctg gag tct ggg atg cag aac atg agt att cat acg aag acc acc       1307
Arg Leu Glu Ser Gly Met Gln Asn Met Ser Ile His Thr Lys Thr Thr
400                    405                    410                    415

agc ggc tat gca ggt ggt ctg agc tcg gcc tat ggg ggc ctc aca agc       1355
Ser Gly Tyr Ala Gly Gly Leu Ser Ser Ala Tyr Gly Gly Leu Thr Ser
                420                    425                    430

ccc ggc ctc agc tac agc ctg ggc tcc agc ttt ggc tct ggc gcg ggc       1403
Pro Gly Leu Ser Tyr Ser Leu Gly Ser Ser Phe Gly Ser Gly Ala Gly
                435                    440                    445

tcc agc tcc ttc agc cgc acc agc tcc tcc agg gcc gtg gtt gtg aag       1451
Ser Ser Ser Phe Ser Arg Thr Ser Ser Ser Arg Ala Val Val Val Lys
        450                    455                    460

aag atc gag aca cgt gat ggg aag ctg gtg tct gag tcc tct gac gtc       1499
Lys Ile Glu Thr Arg Asp Gly Lys Leu Val Ser Glu Ser Ser Asp Val
    465                    470                    475

ctg ccc aag tga acagctgcgg cagcccctcc cagcctaccc ctcctgcgct          1551
Leu Pro Lys  *
480
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tgaggctcag ccctagccct cagcccacct ggggagttta ctacctgggg accccccttg     1671
cccatgcctc cagctacaaa acaattcaat tgcttttttt ttttggtcca aaataaaacc     1731
tcagctagct ctgccaaacc c                                               1752
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<212> PRT
<213> H. sapiens

<400> 4

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            20                  25                  30
Ser Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly Gly
         35                  40                  45
Leu Gly Gly Gly Tyr Gly Gly Ala Ser Gly Met Gly Gly Ile Thr Ala
     50                  55                  60
Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val Asp
65                  70                  75                  80
Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys Thr
                85                  90                  95
Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu Glu
            100                 105                 110
Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln Gln
         115                 120                 125
Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile Asn
     130                 135                 140
Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys Leu
145                 150                 155                 160
Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys Asn
                165                 170                 175
Lys Tyr Glu Asp
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